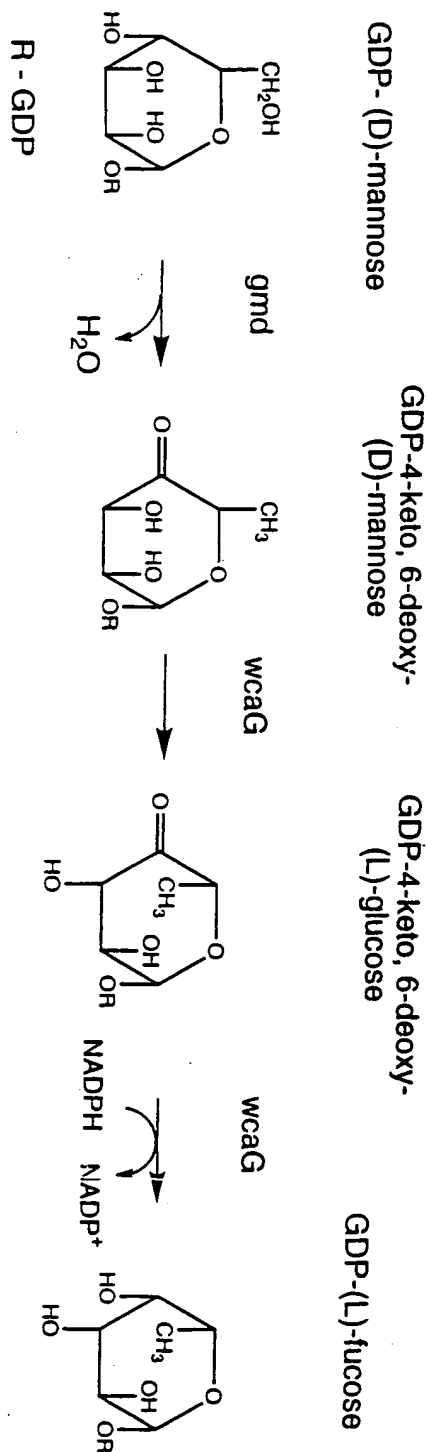


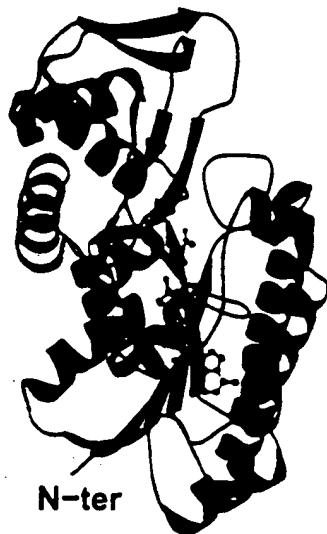


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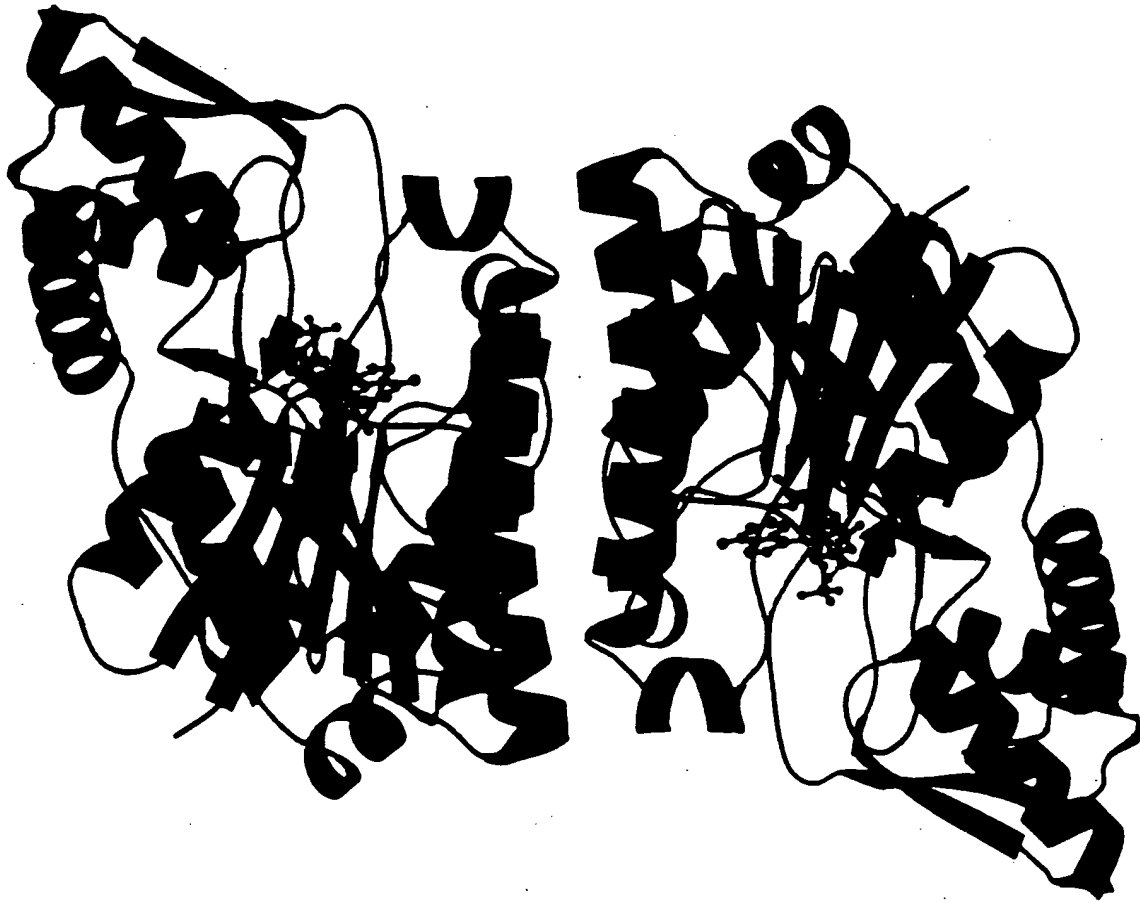


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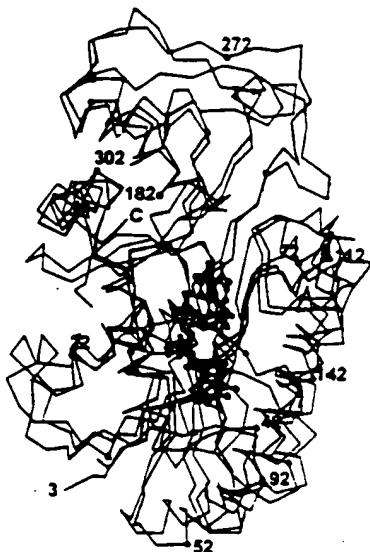


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```
gale      1  -MRVLVT...SGYIGSHTCVQLONG-HDVIIIDNLC...KRSVLPVIERLGGKEPTFVEGD
coli_GFS  3  KQRFVFIAGHGEVGSATRRQLEQNGDVEIHLRTR-----DELN
human_GFS 8  -MRILVTGSGSLVCRAIQNVVADCAQLPGEDWVF-----VSSKDAD
consensus 1  .....

gale      59  IRNEALMTEILHDHAIDTVHIFAGLKA-VGESVQKPLEYDNNVNGTLRLTSAMRAAMVK
coli_GFS  41  LLDGRAVHDFEASERIDQVYLAARVCGIVANNTPADSTYQNHMHESNLIHAHQNDVN
human_GFS 48  LTDTAQTRALPEKVQPTHVHLAAEVGGLFRNKKYNLDGWRKNVENDNVLHSAFEVGAR
consensus 61  .....

gale      118  NFIESSSATVVGCDNPKIPYVES-FPTGTEQ---SPYCKSKLEVEQHLTDLQKAQPDWSIA
coli_GFS  101  KLLPLGSSCIYPKLARQPMASEELQGTLEPTNEPYATKLAGIQLCESYNRQY-GRDYR
human_GFS 108  KVVSCSLSTCIPFDKTTYPIDETHHENGPPHNSNFGYSYARRMIDVQNRAYFOQY-GCTET
consensus 121 .....

gale      174  LERYFNPFVGAHPSGDMGEDPQGIPINNLEBYIAQVAVGR----RDSLAIEGNDYPTEDGTG
coli_GFS  160  SVMPTNLYGPH-----DNFHPNSNHVIPALLRRFDEATAQNAPDVVWGS-----GTF
human_GFS 167  AVIPTNVFGPHDNF-----NIEDGHVLEGLIHRVELAKS-SGSALTVWGTG-----NE
consensus 181 .....

gale      230  VRDYIHVMDLADGHVVAHEKLANK-----EGVETYNLGAQVGMVSLDVVNAFSKACGKP
coli_GFS  208  MREPLHVDDMAASIEHVMELAEVWLENTQPMLSHINVGTCVDCTIRELAQTHARVVGK
human_GFS 214  RRQFIYSLDLAQLFWVIREYNE-----VEPIILSVGEEDVSIKEAAAEAVVEANDEH
consensus 241 .....

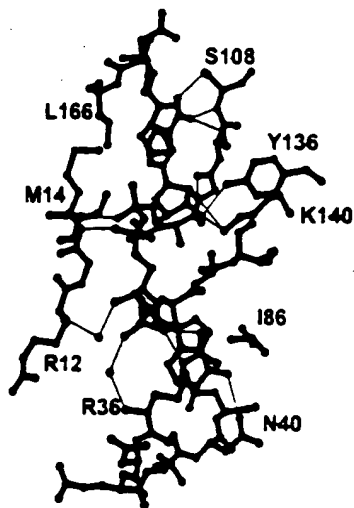
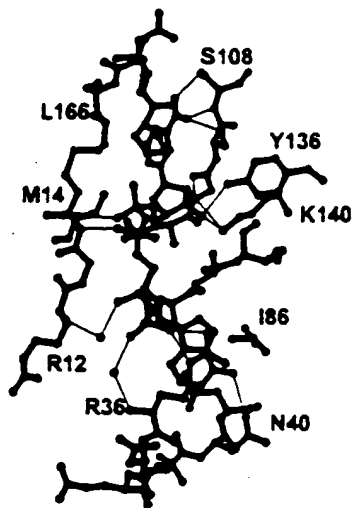
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coli_GFS  268  GRUVFDASKPDGTPRRLLDVRRLHQ-LGWYHEISLEAGLASTYQWFLENQDRF
human_GFS 267  GEVTFDTRKSDGQPKKTASNSKLRTYLPDERFTPFKQAVKETCAWFTDNYEQARK
consensus 301 .....
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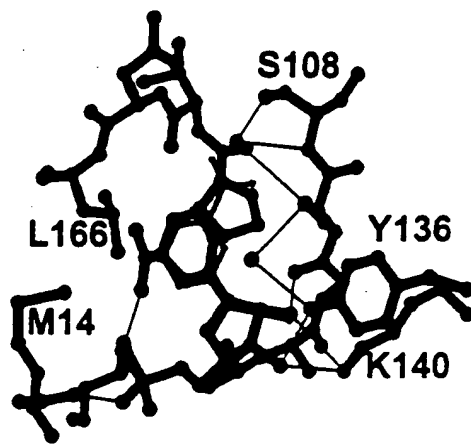
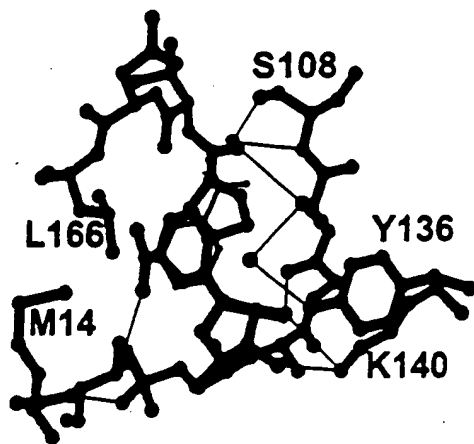




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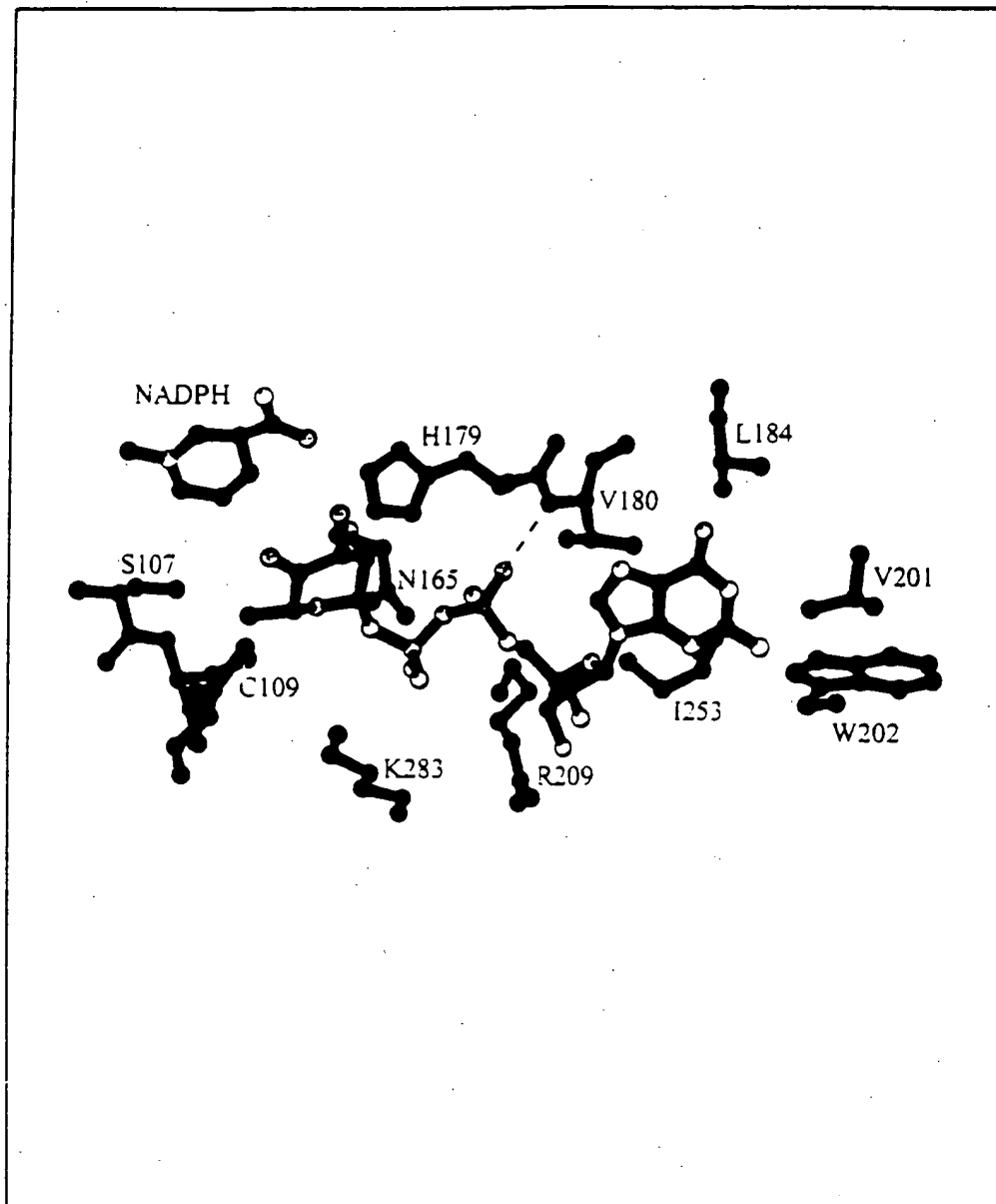
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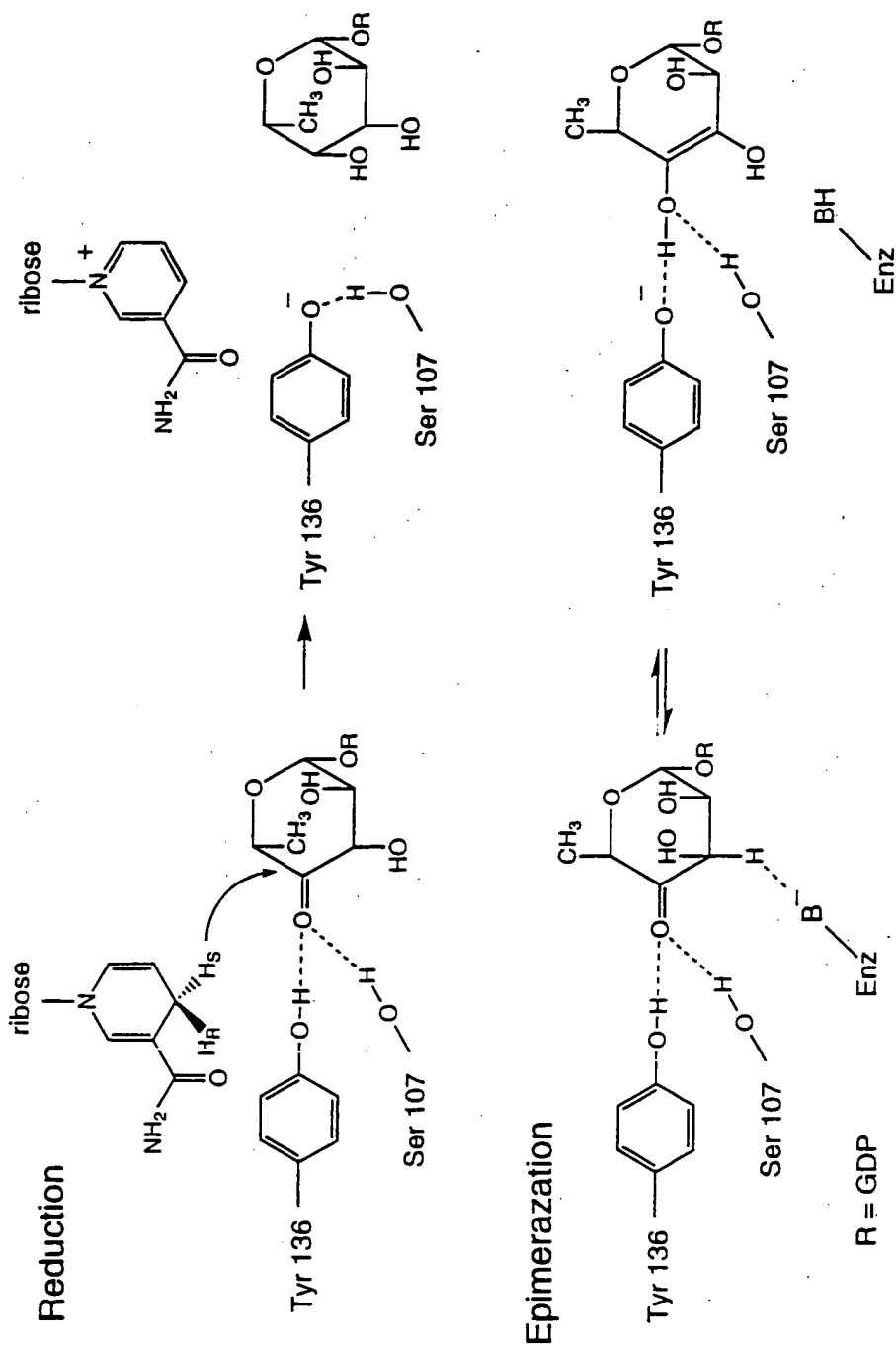
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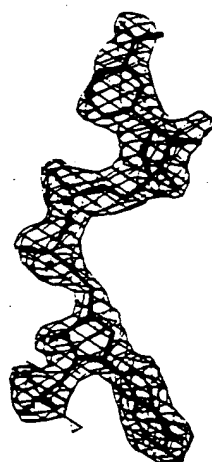
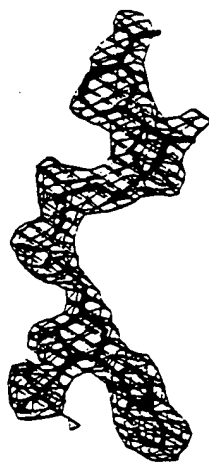


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